AMENDMENT TO THE CLAIMS

WHAT IS CLAIMED IS:

1. (original) A system of analyzing cancers using a proteome image mining tool, comprising:

input means for inputting serum proteome;

proteome standard production means for generating a proteome standard by transforming received serum proteome from a plurality of normal and diseased individuals into two-dimensional images and extracting spots as cancer-specific features from the images, and distinguishing optimal feature data among the extracted feature data, and transforming serum proteome of a subject into a two-dimensional image and extracting features from the image;

proteome comparison means for mapping the serum proteome pattern of the subject, extracted by the proteome standard production means, with the proteome standard pattern to determine similarity between the two patterns;

disease analysis means for estimating the serum proteome of the subject as 'normal' if the serum proteome pattern of the subject would be similar to that of the normal individuals, and otherwise, as 'having cancer', based on the mapping results by the proteome comparison means; and

output means for outputting the analysis results by the disease analysis means.

2. (original) The system as set forth in claim 1, wherein the cancers are selected from the group consisting of breast cancer, ovarian cancer, stomach cancer, liver cancer, uterine cancer, lung cancer, large intestine cancer, pancreatic cancer, or prostate cancer.

3. (original) The system as set forth in claim 1, wherein the proteome standard is one or more selected from spots listed in Table 1.

4. (original) The system as set forth in any of claims 1 to 3, wherein the proteome standard production means distinguishes the feature data by extracting and normalizing correlations between spots comprising the proteome standard.

5. (original) The system as set forth in any of claims 1 to 3, wherein the disease analysis means predicts progression status and future prognosis of cancer when the subject is identified as

having cancer, and, in case that the subject does not have any cancer, predicts probability of cancer development.

6. (original) The system as set forth in any of claims 1 to 3, wherein the system of analyzing cancers further comprises coding means for coding personal information of normal individuals and individuals having cancer, who donate their serum proteomes to be used as standards, and of personal information of subjects.

7. (original) The system as set forth in any of claims 1 to 3, wherein the proteome standard production means comprises pre-processing means for obtaining meaningful feature data from the two-dimensional images of serum proteome, and evolutionary classification means for identifying normality of a serum proteome of a subject from the feature data obtained by said pre-processing means.

8. (original) The system as set forth in claim 7, wherein the proteome standard production means further comprises fuzzy rule-based classification means for extracting correlations between spots contained in the serum proteome from the feature data obtained by the pre-processing means, and classifying the extracted correlations by a statistical method.

9. (original) The system as set forth in claim 8, wherein the fuzzy rule-based classification means comprises data mapping means for computing correlations between spots from the two-dimensional images of serum proteome, classifying the computed features by a statistical technique, and quantifying statistical inaccuracy using a fuzzy technique; and rule-based classification means for arranging and normalizing the results obtained by said data mapping means, and thus generating a rule base.

10. (original) The system as set forth in claim 7, wherein the pre-processing means comprises image processing means for performing general image processing works, including noise filtering, image enhancement, ortho-projection, edge detection and optimal thresholding, from the two-dimensional images of serum proteome, and feature extraction means for extracting features of spots from the image-processed two-dimensional images and labeling each of the features.

11. (original) The system as set forth in claim 7, wherein the evolutionary classification means comprises genetic algorithm processing means for discriminating optimal feature data among the feature data extracted by the pre-processing means, and support vector mechanism

application means for estimating fidelity of the optimal feature data discriminated by said genetic algorithm processing means using estimation functions and a classification error rate.

12. (original) A method of analyzing cancer diseases using a proteome image mining tool, comprising the steps of:

transforming inputted serum proteomes from normal individuals and individuals having cancer into two-dimensional images, extracting feature data from the images, generating a proteome standard by computing optimal features from the feature data, and constructing a database consisting of the proteome standard (Step 1);

inputting a serum proteome from a subject of interest, transforming the serum proteome into a two-dimensional image and extracting feature data from the image (Step 2); and

comparing the structure of the serum proteome pattern of the subject with the proteome standard and determining whether the serum proteome of the subject is normal or abnormal, that is, indicative of cancer (Step 3).

13. (original) The method as set forth in claim 12, wherein the cancer diseases are selected from the group consisting of breast cancer, ovarian cancer, stomach cancer, liver cancer, uterine cancer, lung cancer, large intestine cancer, pancreatic cancer, or prostate cancer.

14. (original) The method as set forth in claim 12, wherein the proteome standard is one or more selected from spots listed in Table 1.

15. (original) The method as set forth in any of claims 12 to 14, wherein the Step 1 further includes the steps of extracting correlations between spots contained in the serum proteome from the two-dimensional images of the serum proteome employing experimental knowledge and a statistical method, and classifying the extracted correlations by a statistical method.

16. (original) The method as set forth in any of claims 12 to 14, wherein the Step 3 further includes a step of identifying present disease states and estimating a future prognosis of the disease by analysing serum proteome of the subject.

17. (original) The method as set forth in any of claims 12 to 14, wherein the Step 3 of identifying the existence (development) of cancer includes:

a pattern matching step of classifying the serum proteome of the subject into "normal" or "having a disease" by applying features and estimation functions, extracted upon producing the proteome standard, to the serum proteome of the subject; and

a fine classification step of deducing fine information including correlations between spots, contained in the two-dimensional proteome images.

18. (original) The method as set forth in any of claims 12 to 14, further comprising a step of constructing a database consisting of the serum proteome of the subject and analysis results thereof, wherein said step is performed after the Step 3.

19. (original) The method as set forth in any of claims 12 to 14, wherein the Step 1 of producing a proteome standard comprises:

a pre-processing step including an image processing step of performing noise filtering, image enhancement, ortho-projection and edge detection from the two-dimensional proteome images, and a feature extraction step of extracting basic features in spot form the image-processed two-dimensional images and producing feature data by labeling each of the extracted features; and

an evolutionary classification step of performing a genetic algorithm to discriminate optimal features playing a critical role in classification among the feature data extracted at the pre-processing step, and extracting optimal feature data and estimation functions by estimating fidelity of the optimal feature data discriminated by the genetic algorithm by a support vector machine using estimation functions and classification error rates.

20. (original) The method as set forth in claim 19, wherein the Step 1 of producing a proteome standard further comprises:

a fuzzy data mapping step of computing correlations between spots from the two-dimensional images of serum proteomes obtained at the pre-processing step, and classifying the computed features by a statistical method, and quantifying statistical inaccuracy using a fuzzy technique; and

a rule-based classification step of arranging and normalizing the results obtained at the data mapping step, and thus generating a final rule base.

21-22. (canceled)